

# Job Submission Status & Plans

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# Outline

## I. DAG/SAM/Job Submission Overview

- Full documentation and usage examples for SAM/DAG/jobsub integration
  - <http://minerva-docdb.fnal.gov/cgi-bin/ShowDocument?docid=7936>

## II. Job Submission Future Plans Overview

- More detailed plan for where job submission is headed here:
  - <http://cd-docdb.fnal.gov/cgi-bin/ShowDocument?docid=4789>

# I. DAG/SAM/Job Submission

- Jobsub\_tools: a KITS product intended to replace minerva\_jobsub and its support scripts
- Jobsub v0\_6 implements SAM/DAG feature
  - Jobsub -h lists options by functional groups, the SAM Options group:

SAM Options:

`--dataset_definition=DATASET_DEFINITION`

SAM dataset definition used in a Directed Acyclic  
Graph (DAG)

`--project_name=PROJECT_NAME`

optional project name for SAM DAG

# Usage Example:

## submitting the script in a DAG

```
$ source /grid/fermiapp/products/minerva/etc/setups.sh
$ setup jobsub_tools
```

```
$ jobsub --dataset_definition mwm_test_2 -N 4 ./consume_sam.sh
/minerva/app/users/condor-tmp/dbbox/consume_sam.sh_20120814_110640_21721_1.dag
submitting....
Submitting job(s).
Logging submit event(s).
1 job(s) submitted to cluster 3997196.
```

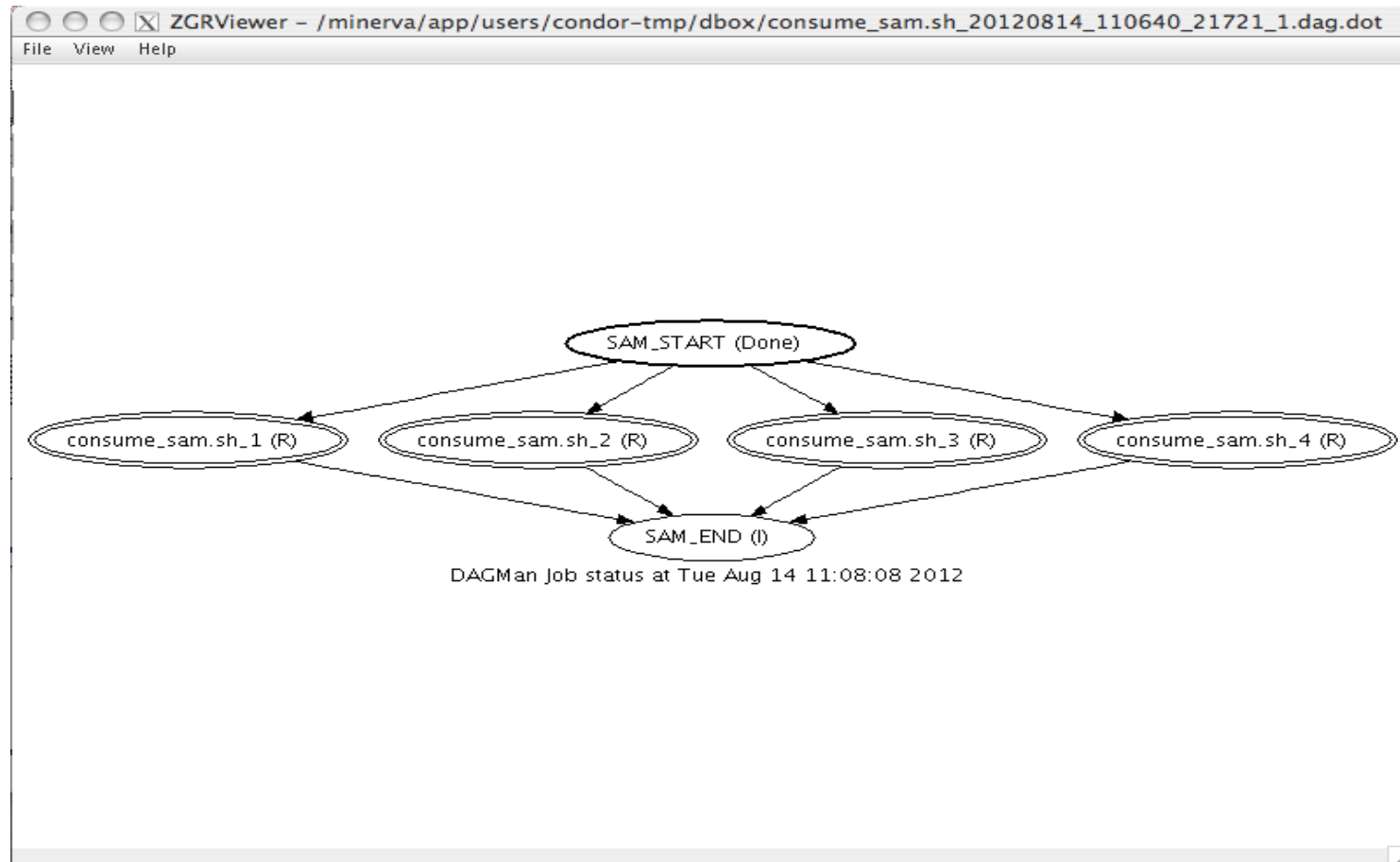
---

```
File for submitting this DAG to Condor      : /minerva/app/users/condor-
tmp/dbbox/consume_sam.sh_20120814_110640_21721_1.dag.condor.sub
Log of DAGMan debugging messages           : /minerva/app/users/condor-
tmp/dbbox/consume_sam.sh_20120814_110640_21721_1.dag.dagman.out
Log of Condor library output               : /minerva/app/users/condor-
tmp/dbbox/consume_sam.sh_20120814_110640_21721_1.dag.lib.out
Log of Condor library error messages       : /minerva/app/users/condor-
tmp/dbbox/consume_sam.sh_20120814_110640_21721_1.dag.lib.err
Log of the life of condor_dagman itself    : /minerva/app/users/condor-
tmp/dbbox/consume_sam.sh_20120814_110640_21721_1.dag.dagman.log
```

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# Monitoring:

- Web page showing progress of file consumption:
  - [http://d0dbweb.fnal.gov:8080/station\\_monitor/minerva/stations/](http://d0dbweb.fnal.gov:8080/station_monitor/minerva/stations/)
- Zrgview command to view DAG progress
  - Jobsub writes DAG filename to stdout
  - Zrgview command runs on DOT file with same name as DAG file with .dot extension
  - `export WHERE=/grid/fermiapp/common/graphviz/zgrviewer/`
  - `$WHERE/zrgview /minerva/app/users/condor-tmp/dbox/consume_sam.sh_20120814_110640_21721_1.dag.dot`



# II. Job Submission Future Plans

## Goals

- Support multiple experiments and submission points

## Realities (Constraints)

- Underlying architecture changes whether we want it to or not
- Experiment interfaces tend to freeze, development resources get reassigned

# Future Plans (cont)

## Strategy

- Standardize as much as possible
  - Can we get rid of `minos_jobsub`, `nova_jobsub`, `minerva_jobsub` and have everyone use the same `jobsub`?
  - If not, we can change `exp_jobsub` to be a wrapper that does experiment specific stuff and then calls `jobsub`
- Abstract as much as possible
  - The `jobsub` scripts are currently `condor` and `bluearc` centric
  - Keep interfaces but hide details so we can change when its forced on us.

# Short term

- Standardization steps
  - jobsub\_tools KITS product contains jobsub, minerva\_jobsub, dagNabbit.py and friends
  - Scripts in 'old' location to be modified to urge users to migrate to new location
  - Requested features will be available in new location, encouraging faster migration



# Longer Term

Full explanation at

<http://cd-docdb.fnal.gov/cgi-bin/ShowDocument?docid=4789>

- Tarball submission – no bluearc needed to run
- Improved execution wrapper
  - Better coupling with monitoring web page/client
  - Communicates with output file server
- Output file server
  - Files sent to spool area
  - Output server handles transfer/change ownership
  - Reduces strain and dependency on bluearc
- Full client server submission architecture
  - Makes it much easier when we have to change back-end batch system
- Better queue implementation
  - (experiment) short, medium, long run times